



SEQUENCE LISTING

<110> LITTLE, MELVYN
KIPRIYANOV, SERGEY
MOLDENHAUER, GERHARD
DEUTSCHES KREBSFORSCHUNGSZENTRUM

<120> MUTATED OKT3 ANTIBODY

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<140> 09/424,705

<141> 2000-06-02

<150> PCT/DE98/01409

<151> 1998-05-22

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<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (28)...(900)

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Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
10 15 20 25

ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag 150
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
30 35 40

atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac 198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
45 50 55

tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att 246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
60 65 70

aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag 294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
75 80 85

| | |
|---|-----|
| gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu 90 95 100 105 | 342 |
| agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr 110 115 120 | 390 |
| tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu 125 130 135 | 438 |
| aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe 140 145 150 | 486 |
| tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met 155 160 165 | 534 |
| tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser 170 175 180 185 | 582 |
| agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro 190 195 200 | 630 |
| aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala 205 210 215 | 678 |
| cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser 220 225 230 | 726 |
| ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser 235 240 245 | 774 |
| agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg 250 255 260 265 | 822 |
| gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu 270 275 280 | 870 |
| gac cta aac tca cat cac cat cac cat cac taatctaga Asp Leu Asn Ser His His His His His His 285 290 | 909 |

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20 25 30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65 70 75 80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
115 120 125
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
130 135 140
Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
145 150 155 160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
165 170 175
Val Thr Met Thr Cys Ser Ala Ser Ser Val Ser Tyr Met Asn Trp
180 185 190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
195 200 205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
210 215 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225 230 235 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
245 250 255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
260 265 270
Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
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His His His
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Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln

102

| 10 | 15 | 20 | 25 | |
|---|-----|----|----|--|
| ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag | 150 | | | |
| Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys | | | | |
| 30 35 40 | | | | |
| atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac | 198 | | | |
| Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His | | | | |
| 45 50 55 | | | | |
| tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att | 246 | | | |
| Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile | | | | |
| 60 65 70 | | | | |
| aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag | 294 | | | |
| Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys | | | | |
| 75 80 85 | | | | |
| gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg | 342 | | | |
| Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met | | | | |
| 90 95 100 105 | | | | |
| caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca | 390 | | | |
| Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala | | | | |
| 110 115 120 | | | | |
| aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc | 438 | | | |
| Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr | | | | |
| 125 130 135 | | | | |
| act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat | 486 | | | |
| Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp | | | | |
| 140 145 150 | | | | |
| atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag | 534 | | | |
| Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln | | | | |
| 155 160 165 | | | | |
| agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt | 582 | | | |
| Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly | | | | |
| 170 175 180 185 | | | | |
| gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa | 630 | | | |
| Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys | | | | |
| 190 195 200 | | | | |
| ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg | 678 | | | |
| Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg | | | | |
| 205 210 215 | | | | |
| ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct | 726 | | | |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro | | | | |
| 220 225 230 | | | | |
| gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag | 774 | | | |
| Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu | | | | |
| 235 240 245 | | | | |

E1

gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct 822
Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
250 255 260 265

cta aac tca cat cac cat cac cat cac taaagatct 906
Leu Asn Ser His His His His His His
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 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
 10 15 20 25

ctg cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag 150
 Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys
 30 35 40

att tcc tgc aag gct tct ggc tat gca ttc agt agc tac tgg atg aac 198
 Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn
 45 50 55

tgg gtg aag cag agg cct gga cag ggt ctt gag tgg att gga cag att 246
 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile
 60 65 70

tgg cct gga gat ggt gat act aac tac aat gga aag ttc aag ggt aaa 294
 Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys
 75 80 85

gcc act ctg act gca gac gaa tcc tcc agc aca gcc tac atg caa ctc 342
 Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu
 90 95 100 105

agc agc cta gca tct gag gac tct gcg gtc tat ttc tgt gca aga cgg 390
 Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg
 110 115 120

gag act acg acg gta ggc cgt tat tac tat gct atg gac tac tgg ggt 438
 Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
 125 130 135

caa gga acc tca gtc acc gtc tcc tca gcc aaa aca aca ccc aag ctt 486
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu
 140 145 150

ggc ggt gat atc gtg ctc act cag tct cca gca atc atg tct gca tct 534
 Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
 155 160 165

cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca agt gta agt 582

E1

| | |
|---|-----|
| Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser | |
| 170 175 180 185 | |
| tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg | 630 |
| Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp | |
| 190 195 200 | |
| att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cac ttc agg | 678 |
| Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg | |
| 205 210 215 | |
| ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc ggc atg gag | 726 |
| Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu | |
| 220 225 230 | |
| gct gaa gat gct gcc act tat tac tgc cag cag tgg agt agt aac cca | 774 |
| Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro | |
| 235 240 245 | |
| ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg gct gat act | 822 |
| Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr | |
| 250 255 260 265 | |
| gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa gac cta aac | 870 |
| Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn | |
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| tca cat cac cat cac cat cac taatctaga | 900 |
| Ser His His His His His His | |
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<400> 6

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| 20 25 30 | |
| Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly | |
| 35 40 45 | |
| Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly | |
| 50 55 60 | |
| Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr | |
| 65 70 75 80 | |
| Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu | |
| 85 90 95 | |
| Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp | |
| 100 105 110 | |
| Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg | |
| 115 120 125 | |
| Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val | |
| 130 135 140 | |
| Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Val Leu Thr | |

| | | | | | | |
|---|-----|-----|-----|-----|-----|-----|
| 145 | | 150 | | 155 | | 160 |
| Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met | | | | | | |
| | 165 | | 170 | | 175 | |
| Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln | | | | | | |
| | 180 | | 185 | | 190 | |
| Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu | | | | | | |
| | 195 | | 200 | | 205 | |
| Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser | | | | | | |
| | 210 | | 215 | | 220 | |
| Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr | | | | | | |
| | 225 | | 230 | | 235 | |
| Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr | | | | | | |
| | 245 | | 250 | | 255 | |
| Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln | | | | | | |
| | 260 | | 265 | | 270 | |
| Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His His His | | | | | | |
| | 275 | | 280 | | 285 | |

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24

<210> 8
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<400> 8
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32

<210> 9
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 <212> DNA
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<400> 9
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32

<210> 10
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 <212> DNA
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<400> 10
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38

<210> 11
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 11
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38

E1